



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lau, Lester F.

(ii) TITLE OF INVENTION: Extracellular Matrix Signalling Molecules

(iii) NUMBER OF SEQUENCES: 21

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Howrey Simon Arnold & White LLP  
(B) STREET: 321 North Clark Street, Suite 3400  
(C) CITY: Chicago  
(D) STATE: Illinois  
(E) COUNTRY: United States of America  
(F) ZIP: 60610

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 10/053,753  
(B) FILING DATE: January 22, 2002  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Clough, David W.  
(B) REGISTRATION NUMBER: 36,107  
(C) REFERENCE/DOCKET NUMBER: 05031.0003.CNUS02

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 312/595-1408  
(B) TELEFAX: 312/595-2250  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1480 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 180..1316

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(D) OTHER INFORMATION: "Mouse cyr61 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGAGCGCC CCAGAGAACGC GCCTGCAATC TCTGCGCCTC CTCCGCCAGC ACCTCGAGAG	60
AAGGACACCC GCGGCCTCGG CCCTCGCCTC ACCGCACTCC GGGCGCATTG GATCCCGCTG	120
CTCGCCGGCT TGTTGGTTCT GTGTCGCCGC GCTCGCCCCG GTTCCTCCTG CGGCCACA	179
ATG AGC TCC AGC ACC TTC AGG ACG CTC GCT GTC GCC GTC ACC CTT CTC Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu	227
1 5 10 15	
CAC TTG ACC AGA CTG GCG CTC TCC ACC TGC CCC GCC TGC CAC TGC His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys	275
20 25 30	
CCT CTG GAG GCA CCC AAG TGC GCC CCG GGA GTC GGG TTG GTC CGG GAC Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp	323
35 40 45	
GGC TGC GGC TGC TGT AAG GTC TGC GCT AAA CAA CTC AAC GAG GAC TGC Gly Cys Gly Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys	371
50 55 60	
AGC AAA ACT CAG CCC TGC GAC CAC ACC AAG GGG TTG GAA TGC AAT TTC Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe	419
65 70 75 80	
GGC GCC AGC TCC ACC GCT CTG AAA GGG ATC TGC AGA GCT CAG TCA GAA Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu	467
85 90 95	
GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA AGC Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser	515
100 105 110	
TTC CAG CCC AAC TGT AAA CAC CAG TGC ACA TGT ATT GAT GGC GCC GTG Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val	563
115 120 125	
GGC TGC ATT CCT CTG TGT CCC CAA GAA CTG TCT CTC CCC AAT CTG GGC Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly	611
130 135 140	
TGT CCC AAC CCC CGG CTG GTG AAA GTC AGC GGG CAG TGC TGT GAA GAG Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu	659
145 150 155 160	
TGG GTT TGT GAT GAA GAC AGC ATT AAG GAC TCC CTG GAC GAC CAG GAT Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp	707
165 170 175	
GAC CTC CTC GGA CTC GAT GCC TCG GAG GTG GAG TTA ACG AGA AAC AAT Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn	755
180 185 190	

GAG TTA ATC GCA ATT GGA AAA GGC AGC TCA CTG AAG AGG CTT CCT GTC Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val 195 200 205	803
TTT GGC ACC GAA CCG CGA GTT CTT TTC AAC CCT CTG CAC GCC CAT GGC Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly 210 215 220	851
CAG AAA TGC ATC GTT CAG ACC ACG TCT TGG TCC CAG TGC TCC AAG AGC Gln Lys Cys Ile Val Gln Thr Ser Trp Ser Gln Cys Ser Lys Ser 225 230 235 240	899
TGC GGA ACT GGC ATC TCC ACA CGA GTT ACC AAT GAC AAC CCA GAG TGC Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys 245 250 255	947
CGC CTG GTG AAA GAG ACC CGG ATC TGT GAA GTG CGT CCT TGT GGA CAA Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln 260 265 270	995
CCA GTG TAC AGC AGC CTA AAA AAG GGC AAG AAA TGC AGC AAG ACC AAG Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys 275 280 285	1043
AAA TCC CCA GAA CCA GTC AGA TTT ACT TAT GCA GGA TGC TCC AGT GTC Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val 290 295 300	1091
AAG AAA TAC CGG CCC AAA TAC TGC GGC TCC TGC GTA GAT GGC CGG TGC Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys 305 310 315 320	1139
TGC ACA CCT CTG CAG ACC AGA ACT GTG AAG ATG CGG TTC CGA TGC GAA Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu 325 330 335	1187
GAT GGA GAG ATG TTT TCC AAG AAT GTC ATG ATG ATC CAG TCC TGC AAA Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys 340 345 350	1235
TGT AAC TAC AAC TGC CCG CAT CCC AAC GAG GCA TCG TTC CGA CTG TAC Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr 355 360 365	1283
AGC CTA TTC AAT GAC ATC CAC AAG TTC AGG GAC TAAGTGCCTC CAGGGTTCCT Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp 370 375	1336
AGTGTGGGCT GGACAGAGGA GAAGCGCAAG CATCATGGAG ACGTGGGTGG GCGGAGGATG	1396
AATGGTGCCT TGCTCATTCT TGAGTAGCAT TAGGGTATTT CAAACTGCC AAGGGCTGA	1456
TGTGGACGGA CAGCAGCGCA GCCG	1480

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (D) OTHER INFORMATION: "Mouse Cyr61 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu  
1 5 10 15

His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys  
20 25 30

Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp  
35 40 45

Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys  
50 55 60

Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe  
65 70 75 80

Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu  
85 90 95

Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser  
100 105 110

Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val  
115 120 125

Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly  
130 135 140

Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu  
145 150 155 160

Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp  
165 170 175

Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn  
180 185 190

Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val  
195 200 205

Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly  
210 215 220

Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser  
225 230 235 240

Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys  
 245 250 255  
 Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln  
 260 265 270  
 Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys  
 275 280 285  
 Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val  
 290 295 300  
 Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys  
 305 310 315 320  
 Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu  
 325 330 335  
 Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys  
 340 345 350  
 Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr  
 355 360 365  
 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp  
 370 375

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1418 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 124..1266
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (D) OTHER INFORMATION: "Human cyr61 cDNA coding sequence"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGCGGGCC	ACCGCGACAC	CGCGCCGCCA	CCCCGACCCC	GCTGCGCACG	GCCTGTCCGC	60
TGCACACCA	G CTTGTTGGCG	TCTTCGTCGC	CGCGCTCGCC	CCGGGCTACT	CCTGCGCGCC	120
ACA ATG AGC TCC CGC ATC GCC AGG GCG CTC GCC TTA GTC GTC ACC CTT						168
Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu	1	5	10	15		
CTC CAC TTG ACC AGG CTG GCG CTC TCC ACC TGC CCC GCT GCC TGC CAC						216
Leu His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His						

	20	25	30	
TGC CCC CTG GAG GCG CCC AAG TGC GCG CCG GGA GTC GGG CTG GTC CGG Cys Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg	35	40	45	264
GAC GGC TGC GGC TGC TGT AAG GTC TGC GCC AAG CAG CTC AAC GAG GAC Asp Gly Cys Gly Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp	50	55	60	312
TGC AGC AAA ACG CAG CCC TGC GAC CAC ACC AAG GGG CTG GAA TGC AAC Cys Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn	65	70	75	360
TTC GGC GCC AGC TCC ACC GCT CTG AAG GGG ATC TGC AGA GCT CAG TCA Phe Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser	80	85	90	408
GAG GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA Glu Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu	100	105	110	456
AGT TTC CAG CCC AAC TGT CAA CAT CAG TGC ACA TGT ATT GAT GGC GCC Ser Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala	115	120	125	504
GTG GGC TGC ATT CCT CTG TGT CCC CAA GAA CTA TCT CTC CCC AAC TTG Val Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu	130	135	140	552
GGC TGT CCC AAC CCT CGG CTG GTC AAA GTT ACC GGG CAG TGC TGC GAG Gly Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu	145	150	155	600
GAG TGG GTC TGT GAC GAG GAT AGT ATC AAG GAC CCC ATG GAG GAC CAG Glu Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln	160	165	170	648
GAC GGC CTC CTT GGC AAG GAG CTG GGA TTC GAT GCC TCC GAG GTG GAG Asp Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu	180	185	190	696
TTG ACG AGA AAC AAT GAA TTG ATT GCA GTT GGA AAA GGC AGA TCA CTG Leu Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu	195	200	205	744
AAG CGG CTC CCT GTT TTT GGA ATG GAG CCT CGC ATC CTA TAC AAC CCT Lys Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro	210	215	220	792
TTA CAA GGC CAG AAA TGT ATT GTT CAA ACA ACT TCA TGG TCC CAG TGC Leu Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys	225	230	235	840
TCA AAG ACC TGT GGA ACT GGT ATC TCC ACA CGA GTT ACC AAT GAC AAC Ser Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn	240	245	250	888
			255	

CCT GAG TGC CGC CTT GTG AAA GAA ACC CGG ATT TGT GAG GTG CGG CCT Pro Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro 260 265 270	936
TGT GGA CAG CCA GTG TAC AGC AGC CTG AAA AAG GGC AAG AAA TGC AGC Cys Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser 275 280 285	984
AAG ACC AAG AAA TCC CCC GAA CCA GTC AGG TTT ACT TAC GCT GGA TGT Lys Thr Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys 290 295 300	1032
TTG AGT GTG AAG AAA TAC CGG CCC AAG TAC TGC GGT TCC TGC GTG GAC Leu Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp 305 310 315	1080
GGC CGA TGC TGC ACG CCC CAG CTG ACC AGG ACT GTG AAG ATG CGG TTC Gly Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe 320 325 330 335	1128
CGC TGC GAA GAT GGG GAG ACA TTT TCC AAG AAC GTC ATG ATG ATC CAG Arg Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln 340 345 350	1176
TCC TGC AAA TGC AAC TAC AAC TGC CCG CAT GCC AAT GAA GCA GCG TTT Ser Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe 355 360 365	1224
CCC TTC TAC AGG CTG TTC AAT GAC ATT CAC AAA TTT AGG GAC Pro Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp 370 375 380	1266
TAAATGCTAC CTGGGTTTCC AGGGCACACC TAGACAAACA AGGGAGAAGA GTGTCAGAAT	1326
CAGAATCATG GAGAAAATGG GCGGGGGTGG TGTGGGTGAT GGGACTCATT GTAGAAAGGA	1386
AGCCTTCTCA TTCTTGAGGA GCATTAAGGT AT	1418

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 381 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (D) OTHER INFORMATION: "Human Cyr61 amino acid sequence"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu Leu 1 5 10 15
--

His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys  
20 25 30

Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp  
35 40 45

Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys  
50 55 60

Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe  
65 70 75 80

Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu  
85 90 95

Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser  
100 105 110

Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala Val  
115 120 125

Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly  
130 135 140

Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu Glu  
145 150 155 160

Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln Asp  
165 170 175

Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu Leu  
180 185 190

Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu Lys  
195 200 205

Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu  
210 215 220

Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser  
225 230 235 240

Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro  
245 250 255

Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys  
260 265 270

Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys  
275 280 285

Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu  
290 295 300

Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly  
305 310 315 320

Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe Arg  
325 330 335

Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln Ser  
340 345 350

Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe Pro  
355 360 365

Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp  
370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (D) OTHER INFORMATION: "Fisp12 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGCC	GACAACCCCCA	GACGCCACCG	CCTGGAGCGT	CCAGACACCA	ACCTCCGCC	60
CTGTCCGAAT	CCAGGCTCCA	GCCGCGCCTC	TCGTCGCCCTC	TGCACCCCTGC	TGTGCATCCT	120
CCTACCGCGT	CCCGATCATG	CTCGCCTCCG	TCGCAGGTCC	CATCAGCCTC	GCCTTGGTGC	180
TCCTCGCCCT	CTGCACCCGG	CCTGCTACGG	GCCAGGACTG	CAGCGCGCAA	TGTCAGTGCG	240
CAGCCGAAGC	AGCGCCGCAC	TGCCCCGCCG	GCGTGAGCCT	GGTGCTGGAC	GGCTGCGGCT	300
GCTGCCCGGT	CTGCGCCAAG	CAGCTGGGAG	AACTGTGTAC	GGAGCGTGAC	CCCTGCGACC	360
CACACAAGGG	CCTCTTCTGC	GATTTGGCT	CCCCCGCCAA	CCGCAAGATT	GGAGTGTGCA	420
CTGCCAAAGA	TGGTGCACCC	TGTGTCTTCG	GTGGGTCGGT	GTACCGCAGC	GGTGAGTCCT	480
TCCAAAGCAG	CTGCAAATAC	CAATGCACCT	GCCTGGATGG	GGCCGTGGGC	TGCGTGCC	540
TATGCAGCAT	GGACGTGCGC	CTGCCAGCC	CTGACTGCC	CTTCCCAGAGA	AGGGTCAAGC	600
TGCCTGGAA	ATGCTGCAAG	GAGTGGGTGT	GTGACGAGCC	CAAGGACCGC	ACAGCAGTTG	660
GCCCTGCCCT	AGCTGCCTAC	CGACTGGAAG	ACACATTGG	CCCAGACCCA	ACTATGATGC	720
GAGCCAAC	TGCTGGTCCAG	ACACAGAGT	GGAGCGCCTG	TTCTAAGACC	TGTGGAATGG	780
GCATCTCCAC	CCGAGTTACC	AATGACAATA	CCTTCTGCAG	ACTGGAGAAG	CAGAGCCGCC	840
TCTGCATGGT	CAGGCCCTGC	GAAGCTGACC	TGGAGGAAAA	CATTAAGAAG	GGCAAAAGT	900

GCATCCGGAC ACCTAAAATC GCCAAGCCTG TCAAGTTGA GCTTTCTGGC TGCACCAGTG	960
TGAAGACATA CAGGGCTAAG TTCTGCAGGG TGTGCACAGA CGGCCGCTGC TGCACACCGC	1020
ACAGAACAC CACTCTGCCA GTGGAGTTCA AATGCCCGA TGGCGAGATC ATGAAAAGA	1080
ATATGATGTT CATCAAGACC TGTGCCTGCC ATTACAAC TGCTGGGAC AATGACATCT	1140
TTGAGTCCCT GTACTACAGG AAGATGTACG GAGACATGGC GTAAAGCCAG GAAGTAAGGG	1200
ACACGAACTC ATTAGACTAT AACTTGAAC GAGTTGCATC TCATTTCTT CTGTAAAAAC	1260
AATTACAGTA GCACATTAAT TTAAATCTGT GTTTTAACT ACCGTGGGAG GAACTATCCC	1320
ACCAAAGTGA GAACGTTATG TCATGGCCAT ACAAGTAGTC TGTCAACCTC AGACACTGGT	1380
TTCGAGACAG TTTACACTTG ACAGTTGTT ATTAGCGCAC AGTGCCAGAA CGCACACTGA	1440
GGTGAGTCTC CTGGAACAGT GGAGATGCCA GGAGAAAGAA AGACAGGTAC TAGCTGAGGT	1500
TATTTAAAAA GCAGCAGTGT GCCTACTTTT TGGAGTGTAA CCGGGGAGGG AAATTATAGC	1560
ATGCTTGCAG ACAGACCTGC TCTAGCGAGA GCTGAGCATG TGTCCCTCAC TAGATGAGGC	1620
TGAGTCCAGC TGTTCTTAA GAACAGCAGT TTCAGCCTCT GACCATTCTG ATTCCAGTGA	1680
CACTTGTCAAG GAGTCAGAGC CTTGTCTGTT AGACTGGACA GCTTGTGGCA AGTAAGTTG	1740
CCTGTAACAA GCCAGATTTT TATTGATATT GTAAATATTG TGGATATATA TATATATATA	1800
TATATTGTA CAGTTATCTA AGTTAATTAA AAGTCATTTG TTTTGTTTT AAGTGTCTTT	1860
GGGATTTAA ACTGATAGCC TCAAACCTCA AACACCATAG GTAGGACACG AAGCTTATCT	1920
GTGATTCAA ACAAAAGGAGA TACTGCAGTG GGAATTGTGA CCTGAGTGAC TCTCTGTCAG	1980
AACAAACAAA TGCTGTGCAG GTGATAAAGC TATGTATTGG AAGTCAGATT TCTAGTAGGA	2040
AATGTGGTCA AATCCCTGTT GGTGAACAAA TGGCCTTAT TAAGAAATGG CTGGCTCAGG	2100
GTAAGGTCCG ATTCCTACCA GGAAGTGCTT GCTGCTTCTT TGATTATGAC TGGTTGGGG	2160
TGGGGGGCAG TTTATTTGTT GAGAGTGTGA CCAAAAGTTA CATGTTTGCA CCTTTCTAGT	2220
TGAAAATAAA GTATATATAT ATTTTTATA TGAAAAAAA GGAATTC	2267

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 348 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(D) OTHER INFORMATION: "Fisp12 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Leu Ala Ser Val Ala Gly Pro Ile Ser Leu Ala Leu Val Leu Leu  
1 5 10 15

Ala Leu Cys Thr Arg Pro Ala Thr Gly Gln Asp Cys Ser Ala Gln Cys  
20 25 30

Gln Cys Ala Ala Glu Ala Ala Pro His Cys Pro Ala Gly Val Ser Leu  
35 40 45

Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu Gly  
50 55 60

Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu Phe  
65 70 75 80

Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr Ala  
85 90 95

Lys Asp Gly Ala Pro Cys Val Phe Gly Ser Val Tyr Arg Ser Gly  
100 105 110

Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp Gly  
115 120 125

Ala Val Gly Cys Val Pro Leu Cys Ser Met Asp Val Arg Leu Pro Ser  
130 135 140

Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys Cys  
145 150 155 160

Lys Glu Trp Val Cys Asp Glu Pro Lys Asp Arg Thr Ala Val Gly Pro  
165 170 175

Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr  
180 185 190

Met Met Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys  
195 200 205

Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn  
210 215 220

Thr Phe Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro  
225 230 235 240

Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile  
245 250 255

Arg Thr Pro Lys Ile Ala Lys Pro Val Lys Phe Glu Leu Ser Gly Cys  
260 265 270

Thr	Ser	Val	Lys	Thr	Tyr	Arg	Ala	Lys	Phe	Cys	Gly	Val	Cys	Thr	Asp
275							280					285			
Gly	Arg	Cys	Cys	Thr	Pro	His	Arg	Thr	Thr	Leu	Pro	Val	Glu	Phe	
290							295			300					
Lys	Cys	Pro	Asp	Gly	Glu	Ile	Met	Lys	Lys	Asn	Met	Met	Phe	Ile	Lys
305					310				315				320		
Thr	Cys	Ala	Cys	His	Tyr	Asn	Cys	Pro	Gly	Asp	Asn	Asp	Ile	Phe	Glu
					325				330				335		
Ser	Leu	Tyr	Tyr	Arg	Lys	Met	Tyr	Gly	Asp	Met	Ala				
					340			345							

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2075 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (D) OTHER INFORMATION: "CTGF cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCGGCCGAC	AGCCCCGAGA	CGACAGCCCG	GCGCGTCCCG	GTCCCCACCT	CCGACCACCG	60
CCAGCGCTCC	AGGCCCCGCG	CTCCCCGCTC	GCCGCCACCG	CGCCCTCCGC	TCCGCCCGCA	120
GTGCCAACCA	TGACCGCCGC	CAGTATGGGC	CCCGTCCGCG	TCGCCTTCGT	GGTCCTCCTC	180
GCCCTCTGCA	GCCGGCCGGC	CGTCGGCCAG	AACTGCAGCG	GGCCGTGCCG	GTGCCCGGAC	240
GAGCCGGCGC	CGCGCTGCC	GGCGGGCGTG	AGCCTCGTGC	TGGACGGCTG	CGGCTGCTGC	300
CGCGTCTGCG	CCAAGCAGCT	GGCGAGCTG	TGCACCGAGC	GCGACCCCTG	CGACCCGCAC	360
AAGGGCCTCT	TCTGTGACTT	CGGCTCCCCG	GCCAACCGCA	AGATCGGCGT	GTGCACCGGCC	420
AAAGATGGTG	CTCCCTGCAT	CTTCGGTGGT	ACGGTGTACC	GCAGCGGAGA	GTCCTTCCAG	480
AGCAGCTGCA	AGTACCAGTG	CACGTGCCTG	GACGGGGCGG	TGGGCTGCAT	GCCCCTGTGC	540
AGCATGGACG	TTCGTCTGCC	CAGCCCTGAC	TGCCCCCTTCC	CGAGGGAGGGT	CAAGCTGCC	600
GGGAAATGCT	GCGAGGAGTG	GGTGTGTGAC	GAGCCAAGG	ACCAAACCGT	GGTTGGGCCT	660
GCCCTCGCGG	CTTACCGACT	GGAAAGACACG	TTTGGCCAG	ACCCAACAT	GATTAGAGCC	720
AACTGCCTGG	TCCAGACCAAC	AGAGTGGAGC	GCCTGTTCCA	AGACCTGTGG	GATGGGCATC	780

TCCACCCGGG TTACCAATGA CAACGCCTCC TGCAGGCTAG AGAAGCAGAG CCGCCTGTGC	840
ATGGTCAGGC CTTGCGAAGC TGACCTGGAA GAGAACATTA AGAAGGGCAA AAAGTGCATC	900
CGTACTCCCA AAATCTCCAA GCCTATCAAG TTTGAGCTTT CTGGCTGCAC CAGCATGAAG	960
ACATACCGAG CTAAATTCTG TGGAGTATGT ACCGACGGCC GATGCTGCAC CCCCCACAGA	1020
ACCACCACCC TGCCGGTGGAA GTTCAAGTGC CCTGACGGCG AGGTCAATGAA GAAGAACATG	1080
ATGTTCATCA AGACCTGTGC CTGCCATTAC AACTGTCCCG GAGACAATGA CATCTTGAA	1140
TCGCTGTACT ACAGGAAGAT GTACGGAGAC ATGGCATGAA GCCAGAGAGT GAGAGACATT	1200
AACTCATTAG ACTGGAACCTT GAACTGATTC ACATCTCATT TTTCCGTAAA AATGATTCA	1260
GTAGCACAAG TTATTTAAAT CTGTTTTCT AACTGGGGGA AAAGATTCCC ACCCAATTCA	1320
AAACATTGTG CCATGTCAAA CAAATAGTCT ATCTTCCCCA GACACTGGTT TGAAGAATGT	1380
TAAGACTTGAA CAGTGGAACT ACATTAGTAC ACAGCACCAAG AATGTATATT AAGGTGTGGC	1440
TTTAGGAGCA GTGGGAGGGT ACCGGCCCGG TTAGTATCAT CAGATCGACT CTTATACGAG	1500
TAATATGCCT GCTATTTGAA GTGTAATTGA GAAGGAAAAT TTTAGCGTGC TCACTGACCT	1560
GCCTGTAGCC CCAGTGACAG CTAGGATGTG CATTCTCCAG CCATCAAGAG ACTGAGTC	1620
GTTGTTCCCTT AAGTCAGAAC AGCAGACTCA GCTCTGACAT TCTGATTGCA ATGACACTGT	1680
TCAGGAATCG GAATCCTGTC GATTAGACTG GACAGCTTGT GGCAAGTGAA TTTGCCTGTA	1740
ACAAGCCAGA TTTTTTAAAAA TTTATATTGT AAATATTGTG TGTGTGTGTG TGTGTGTATA	1800
TATATATATA TATGTACAGT TATCTAAGTT AATTAAAGT TGGTTGTGCC TTTTTATTTT	1860
TGTTTTAAAT GCTTTGATAT TTCAATGTTA GCCTCAATTT CTGAACACCA TAGGTAGAAT	1920
GTAAAGCTTG TCTGATCGTT CAAAGCATGA AATGGATACT TATATGGAAA TTCTGCTCAG	1980
ATAGAATGAC AGTCCGTCAA AACAGATTGT TTGCAAAGGG GAGGCATCAG TGTCTGGCA	2040
GGCTGATTTC TAGGTAGGAA ATGTGGTAGC TCACG	2075

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (D) OTHER INFORMATION: "CTGF amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu  
1 5 10 15

Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro  
20 25 30

Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser  
35 40 45

Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu  
50 55 60

Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu  
65 70 75 80

Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr  
85 90 95

Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser  
100 105 110

Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp  
115 120 125

Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro  
130 135 140

Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys  
145 150 155 160

Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly  
165 170 175

Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro  
180 185 190

Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala  
195 200 205

Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp  
210 215 220

Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg  
225 230 235 240

Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Cys  
245 250 255

Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly  
260 265 270

Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr  
275 280 285

Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu  
290 295 300  
Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile  
305 310 315 320  
Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe  
325 330 335  
Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala  
340 345

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGATCTGT GACGAGCCCCA AGGAC 25

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGAATTCGA CCAGGCAGTT GGCTCG 26

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGGATCCTG TGATGAAGAC AGCATT

26

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGAATTCAA CGATGCATTT CTGGCC

26

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp  
1 5 10 15

Cys Ser Lys Thr Gln  
20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val Gly Cys  
1 5 10 15  
Ile Pro Leu Cys Pro  
20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser Cys Gly  
1 5 10 15  
Thr Gly Ile Ser Thr Arg Val Thr  
20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys Arg Leu Val Lys  
1 5 10 15  
Glu Thr Arg Ile Cys Glu Val Arg Pro Cys  
20 25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys Cys Thr Pro Leu Gln  
1 5 10 15

Thr Arg Thr Val Lys  
20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

gggaattctg tcgggatctg tctgtcaaga gtgctg 36

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ccggatccga cagattgata gattgaca 28

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Gly Ser Ala Gly Ala Arg Pro Ala Leu Ala Ala Ala Leu Leu Cys  
1 5 10 15  
Leu Ala Arg Leu Ala Leu Gly Ser Pro Cys Pro Ala Val Cys Gln Cys  
20 25 30  
Pro Ala Ala Ala Pro Gln Cys Ala Pro Gly Val Gly Leu Val Pro Asp  
35 40 45  
Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys  
50 55 60  
Ser Arg Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe  
65 70 75 80  
Gly Ala Ser Pro Ala Ala Thr Asn Gly Ile Cys Arg Ala Gln Ser Glu  
85 90 95  
Gly Arg Pro Cys Glu Tyr Asn Ser Lys Ile Tyr Gln Asn Gly Glu Ser  
100 105 110  
Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val  
115 120 125  
Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly  
130 135 140  
Cys Pro Ser Pro Arg Leu Val Lys Val Pro Gly Gln Cys Cys Glu Glu  
145 150 155 160  
Trp Val Cys Asp Glu Ser Lys Asp Ala Leu Glu Glu Leu Glu Gly Phe  
165 170 175  
Phe Ser Lys Glu Phe Gly Leu Asp Ala Ser Glu Gly Glu Leu Thr Arg  
180 185 190  
Asn Asn Glu Leu Ile Ala Ile Val Lys Gly Gly Leu Lys Met Leu Pro  
195 200 205  
Val Phe Gly Ser Glu Pro Gln Ser Arg Ala Phe Glu Asn Pro Lys Cys  
210 215 220  
Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Thr Cys Gly Thr  
225 230 235 240  
Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Asp Cys Lys Leu Ile  
245 250 255  
Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln Pro Ser Tyr  
260 265 270  
Ala Ser Leu Lys Lys Gly Lys Cys Thr Lys Thr Lys Lys Ser Pro  
275 280 285  
Ser Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val Lys Lys Tyr  
290 295 300  
Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys Cys Thr Pro  
305 310 315 320  
Gln Gln Thr Arg Thr Val Lys Ile Arg Phe Arg Cys Asp Asp Gly Glu  
325 330 335  
Thr Phe Thr Lys Ser Val Met Met Ile Gln Ser Cys Arg Cys Asn Tyr  
340 345 350  
Asn Cys Pro His Ala Asn Glu Ala Tyr Pro Phe Tyr Arg Leu Val Asn  
355 360 365  
Asp Ile His Lys Phe Arg Asp  
370 375

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Glu Thr Gly Gly Gln Gly Leu Pro Val Leu Leu Leu Leu  
1 5 10 15  
Leu Leu Leu Arg Pro Cys Glu Val Ser Gly Arg Glu Ala Ala Cys Pro  
20 25 30  
Arg Pro Cys Gly Gly Arg Cys Pro Ala Glu Pro Pro Arg Cys Ala Pro  
35 40 45  
Gly Val Pro Ala Val Leu Asp Gly Cys Gly Cys Leu Val Cys Ala  
50 55 60  
Arg Gln Arg Gly Glu Ser Cys Ser Pro Leu Leu Pro Cys Asp Glu Ser  
65 70 75 80  
Gly Gly Leu Tyr Cys Asp Arg Gly Pro Glu Asp Gly Gly Ala Gly  
85 90 95  
Ile Cys Met Val Leu Glu Gly Asp Asn Cys Val Phe Asp Gly Met Ile  
100 105 110  
Tyr Arg Asn Gly Glu Thr Phe Gln Pro Ser Cys Lys Tyr Gln Cys Thr  
115 120 125  
Cys Arg Asp Gly Gln Ile Gly Cys Leu Pro Arg Cys Asn Leu Gly Leu  
130 135 140  
Leu Leu Pro Gly Pro Asp Cys Pro Phe Pro Arg Lys Ile Glu Val Pro  
145 150 155 160  
Gly Glu Cys Cys Glu Lys Trp Val Cys Asp Pro Arg Asp Glu Val Leu  
165 170 175  
Leu Gly Gly Phe Ala Met Ala Ala Tyr Arg Gln Glu Ala Thr Leu Gly  
180 185 190  
Ile Asp Val Ser Asp Ser Ser Ala Asn Cys Ile Glu Gln Thr Thr Glu  
195 200 205  
Trp Ser Ala Cys Ser Lys Ser Cys Gly Met Gly Phe Ser Thr Arg Val  
210 215 220  
Thr Asn Arg Asn Gln Gln Cys Glu Met Val Lys Gln Thr Arg Leu Cys  
225 230 235 240  
Met Met Arg Pro Cys Glu Asn Glu Glu Pro Ser Asp Lys Lys Gly Lys  
245 250 255  
Lys Cys Ile Gln Thr Lys Lys Ser Met Lys Ala Val Arg Phe Glu Tyr  
260 265 270  
Lys Asn Cys Thr Ser Val Gln Thr Tyr Lys Pro Arg Tyr Cys Gly Leu  
275 280 285  
Cys Asn Asp Gly Arg Cys Cys Thr Pro His Asn Thr Lys Thr Ile Gln  
290 295 300  
Val Glu Phe Arg Cys Pro Gln Gly Lys Phe Leu Lys Lys Pro Met Met  
305 310 315 320  
Leu Ile Asn Thr Cys Val Cys His Gly Asn Cys Pro Gln Ser Asn Asn  
325 330 335

Ala Phe Phe Gln Pro Leu Asp Pro Met Ser Ser Glu Ala Lys Ile  
340 345 350